

Fig. 1A

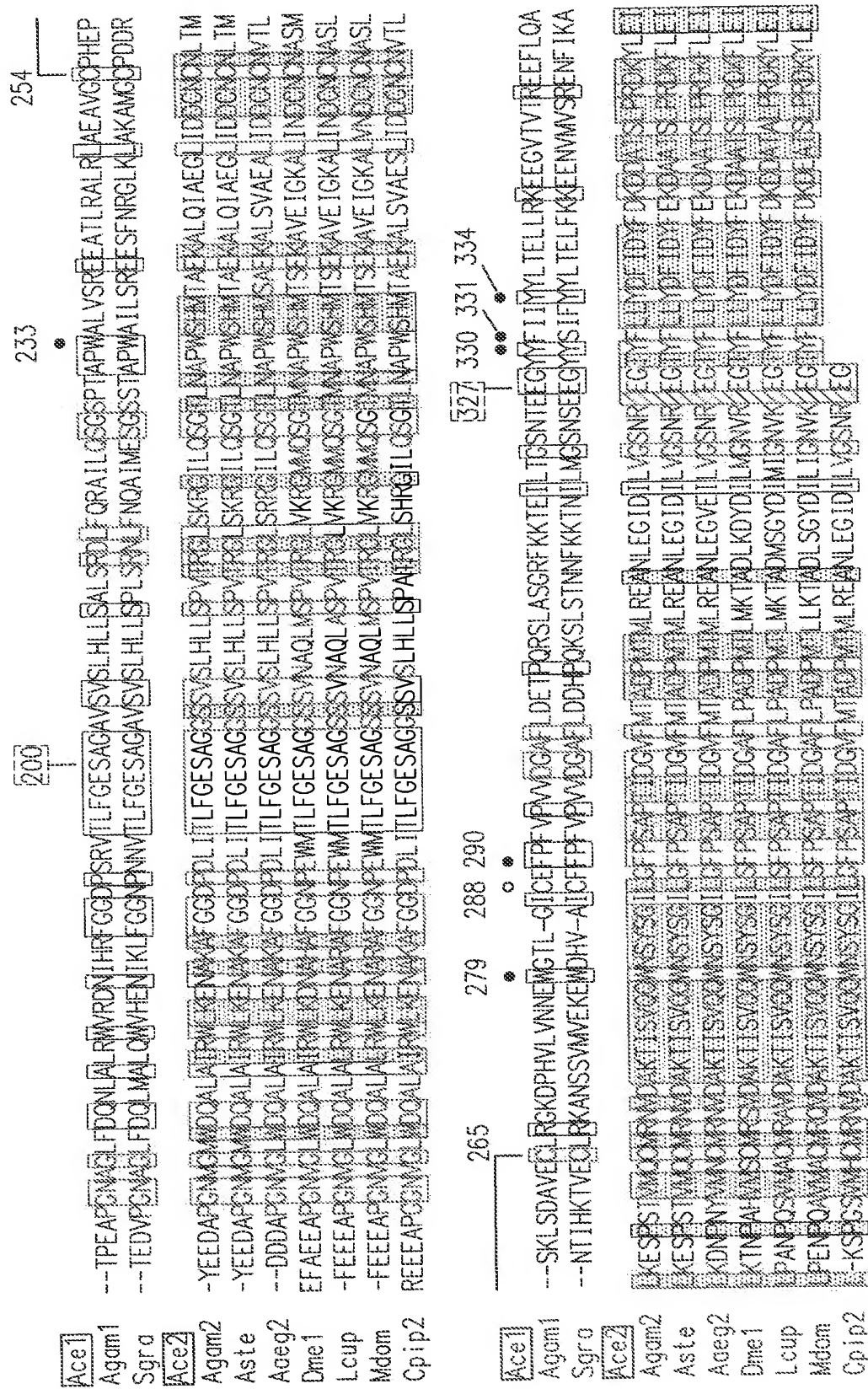


Fig. 1B

PdirACSG

 K fragment

 402
 432
 440-442
 0
 VRELNPYNGAARQAIMFEYIDITEPDNPNSRDALDKMGDYHFTQWMEFAQRYAEESNMVMTLYTHRSKGNPMPRTGSMVHCDEINNVFGEPLNPT
 AGam1
 IGQLNPADAAVKSAIEFEYIDITEPDNPNSRDALDKMGDYHFTQWMEFAQRYAEESNMVMTLYTHRSKGNPMPRTGSMVHCDEISNVFGEPLNPN
 Sgro
 IEPDNPNSRDALDKMGDYHFTQWMEFAQRYAEESNMVMTLYTHRSKGNPMPRTGSMVHCDEINNVFGEPLNSA
 Cpip1
 TEPEPNPNSRDALDKMGDYHFTQWMEFAQRYAEESNMVMTLYTHRSKGNPMPRTGSMVHCDEINNVFGEPLNSD
 Agea1

Ace2
Agam2
Aste
Aceg2
Dme1
Lcup
Mdom

ace2	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523
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Fig. 1C

1 80
Ae alb TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYAEEGNNV YMYLYTHR SK GNPWPRWTGV MHGDEIN YVF GEPLNPSLGY
Ae aeg TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYAEEGNNV YMYLYTHR SK GNPWPRWTGV MHGDEIN YVF GEPLNPSLGY
An alb TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYAEEGNNV YMYLYTHR SK GNPWPRWTGV MHGDEIN YVF GEPLNPSLGY
An gam TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYAEEGNNV YMYLYTHR SK GNPWPRWTGV MHGDEIN YVF GEPLNPSLGY
An fun TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYAEEGNNV YMYLYTHR SK GNPWPRWTGV MHGDEIN YVF GEPLNPSLGY
An nil TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYAEEGNNV YMYLYTHR SK GNPWPRWTGV MHGDEIN YVF GEPLNPSLGY
An sac TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYAEEGNNV YMYLYTHR SK GNPWPRWTGV MHGDEIN YVF GEPLNPSLGY
An pse TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYAEEGNNV YMYLYTHR SK GNPWPRWTGV MHGDEIN YVF GEPLNPSLGY
Cx Pip TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYAEEGNNV YMYLYTHR SK GNPWPRWTGV MHGDEIN YVF GEPLNPSLGY

81 91
Ae alb TEDEKDFSRK I
Ae aeg TEDEKDFSRK I
An alb TEDEKDFSRK I
An gam TEDEKDFSRK I
An fun TEDEKDFSRK I
An nil TEDEKDFSRK I
An sac TEDEKDFSRK I
An pse TEDEKDFSRK I
Cx Pip TEDEKDFSRK I

Fig. 2A

Ace1-SLAB
 Ace1-SR

• 20 • 40 • 60 • 80

ATGACCCGACACCCGACAGCAACCGTGACCGCGCTGGACAAGATGGTCGGGGATTATCATTACCTTCCAACGTGAA
 ATGCAACCCGACACCCGACAGCAACCGTGACCGCGCTGGACAAGATGGTCGGGGATTATCATTACCTTCCAACGTGAA

Ace1-SLAB
 Ace1-SR

EcoRI • 100 • 120 • 140 • 160

CGAATTCGCCCCAGCGGTACGCCGAGGAGGGCAACAACGTGTTCAATGTAACCTGTACACGCCACAGCAAGCAAAAGGAAATCCCT
 CGAATTCGCCCCAGCGGTACGCCGAGGAGGGCAACAATGTGTTCAATGTAACCTGTACACGCCACAGCAAGCAAAAGGAAATCCCT

Ace1-SLAB
 Ace1-SR

• 180 • 200 • 220 • 240

GGCCGAGGTGGACGGGGTGATGCACGGCGACGAGATCAACTACGTGTTTCCGGAACCGCTGAACCTCGGCCCTCGGCTAC
 GGCCGAGGTGGACGGGGTGATGCACGGCGACGAGATCAACTACGTGTTTCCGGAACCGCTGAACCTCGGCCCTCGGCTAC

Ace1-SLAB
 Ace1-SR

• 260 •

CAGGACGACGAGAGGACTTTAGCCGGGAAAATT
 CAGGACGACGAGAGGACTTTAGCCGGGAAAATT

Fig. 2B

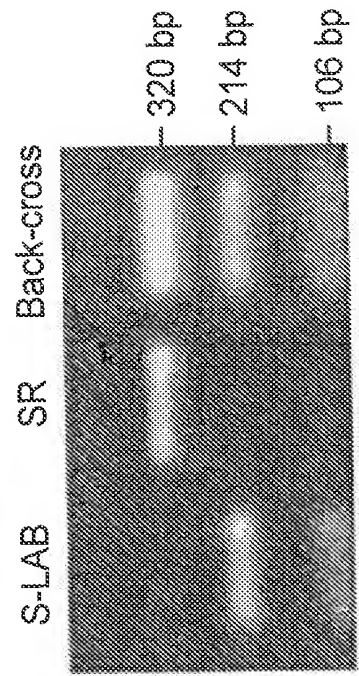


Fig. 2C

80

1 SR MEIRGLITRL LGPCHLRHLI LCSLGLYSIL VQSVHCRHHD IGSSVAHQLG SKYSQSSSL SSSQSSSLA EEATLNKDS
S-LAB MEIRGLITRL LGPCHLRHLI LCSLGLYSIL VQSVHCRHHD IGSSVAHQLG SKYSQSSSL SSSQSSSLA EEATLNKDS

160

81 SR AFFTPYIGHG DSVRIVDAEL GTLEREHIHS ITTTRRRGLR RESSSDATDS DPLVITTDKG KIRGTTLEAP SGKKYDAWNG
S-LAB AFFTPYIGHG DSVRIVDAEL GTLEREHIHS ITTTRRRGLR RESSSDATDS DPLVITTDKG KIRGTTLEAP SGKKYDAWNG

240

161 SR IPYAQPPLGP LRFHRPRPAE RWTGVLNATK PPNSCVQIVD TVFGDFPGAT MNNPTPLSE DCLYINWVP RPRPKNAAVM
S-LAB IPYAQPPLGP LRFHRPRPAE RWTGVLNATK PPNSCVQIVD TVFGDFPGAT MNNPTPLSE DCLYINWVP RPRPKNAAVM

320

241 SR LWIFGCGFYYS GTATLDVYDH RTLASEENVI VWSLQYRVAS LGFLFGTPE APGNAGLFDQ NLALRWVRDN IHRFGGDP
S-LAB LWIFGCGFYYS GTATLDVYDH RTLASEENVI VWSLQYRVAS LGFLFGTPE APGNAGLFDQ NLALRWVRDN IHRFGGDP

400

321 SR VTLFGESAGA VSVSLHLLSA LSRDLFQRAI LQSGSPTAPW ALVSREEATL RALRLAEAVN CPHDATKLSO AVECLRTKDP
S-LAB VTLFGESAGA VSVSLHLLSA LSRDLFQRAI LQSGSPTAPW ALVSREEATL RALRLAEAVN CPHDATKLSO AVECLRTKDP

480

401 SR NELVDNEWGT LGICEFFFPV WDGAFDDET PQSLASGRF KKTIDILIGSN TEEGYFYIY YLTLLRKEE GVTVTREEFL
S-LAB NELVDNEWGT LGICEFFFPV WDGAFDDET PQSLASGRF KKTIDILIGSN TEEGYFYIY YLTLLRKEE GVTVTREEFL

560

481 SR QAVRELNPYV NGAARQAIVF EYTDWIEPDN PNSNRDALK MWDYHFTCN VNEFAQRYAE EGNVFMVLY THRSKGNPWP
S-LAB QAVRELNPYV NGAARQAIVF EYTDWIEPDN PNSNRDALK MWDYHFTCN VNEFAQRYAE EGNVFMVLY THRSKGNPWP

620

561 SR RWTGVMHGDE INYVGEPLN SALGYQDDEK DFSRKIMRYW SNFAKTGNPN PSTPSVDLPE WPKHTAHGRH YLELGLNTTF
S-LAB RWTGVMHGDE INYVGEPLN SALGYQDDEK DFSRKIMRYW SNFAKTGNPN PSTPSVDLPE WPKHTAHGRH YLELGLNTTF

702

621 SR VGRGPRLRQC AFWKKYLPLQL VAATSNLOVT PAPSVPCESS STSYRSTLLL IVTLLLVTRF KI
S-LAB VGRGPRLRQC AFWKKYLPLQL VAATSNLOVT PAPSVPCESS STSYRSTLLL IVTLLLVTRF KI

Fig. 5

125
1 M E I R G L I T R L L G P C H L R H L I L C S L G L Y S I L V Q S V H C R H H D I G
S-Lab ATGGACATCCGAGCCCTAATAACCGATTACTGGGTCCATGTCACTGGGACATCTGATCTGCGGTGTACTCCATCTGCTGCCAGTGGTCCATTCGCGGCATCATGACATCGG
SR
250
126 S V A H Q L G S K Y S Q S S L S S S Q S S S L A E E A T L N K D S D A F F T
S-Lab TAGTTCGGTGGCACACCGCTAGGATCGCAATCAATCACTCAATCACTCCCTTATGCTCATCTGCAATGTCATGCTGTAGCTGAAGAGCCACCGTCGAATAAGATTTCAGATCCATTTTAA
SR
375
375 P Y I G H G D S V R I V D A E L G T L E R E H I H S I T T R R R G L T R R E S S S
S-Lab CACCATATATAGGTACGGAGATTCTGTTGGAATTGTAGATGCCGAATTAGGTACATTAGACGGGAGCCACATCCATAGCACTACGACCCGCGGCTGGCTTGACGGAGGAGTCCAGCTCC
SR
500
376 D A T D S D P L V I T T D K G K I R G T T L E A P S G K K V D A W M G I P Y A Q P P
S-Lab GATGCCACCGACTCGGACCCACTGGTCATAACGACGACAGGCAAAATCCGTGGAAACGACACTGGAAACGCTAGTGAAGAGGTCGACCGCATGGATGGCCATTCCGTACGGCAGCCGCC
SR
Amorce Ex3dir
625
501 L G P L R F R H P R P A E R W T G V L N A T K P P N S C V Q I V D T V F G D F P G A
S-Lab GCTGGGTCCGCTCCGGTTTCGACATCCGGCAAGATGGACCGGTGCTCAACGGACCAACCCCACTCCCTGGTCCAGATGGTGGACACCGTGTTCGGTGACTTCGCGGGGG
SR
750
626 T M W N P N T P L S E D C L Y I N V V V P R P R P K N A A V M L W I F G C F Y S
S-Lab CCACCATCTGGAACCGCAACACACCGCTCTCGGAGGACTGTCTGTACATCAAGCTGGTGGACCGCCAGGCCAAGCAATGCCCGCTCATGCTGGATCTTCGCGGGTGGCTTCTACTCC
SR
-C-----A-----G-----T-----T-----S-----

Fig. 6A

S-Lab SR	875	G T A T L D V Y D H R T L A S E E N V I V V S L Q Y R V A S L G F L F L G T P E A P CGGAC TGGCAGCGCTGACGACATGGCAGCGTGGCTGGAGGAGAGCTGATCGTAGTTTGGCTCCAGTACCGTGGCAAGCTTTCCCTCCGACACCGGAGGCAAC
		-----T-----G-----T-----
S-Lab SR	876	G N A G L F D Q N L A L R W V R D N I H R F G G D P S R V T L F G E S A G A V S V S CGGTAAOCCGCGCTTTGATCAGAACCTTGGACCTGAGATGGTCCGCGACACATCCACCGTTGGGGGTGACCCCTGGCGGTACACATCTGGCCGACAGCCCGGAGCGCTCCGCTTT
		-----T-----
S-Lab SR	1001	L H L L S A L S R D L F Q R A I L Q S G S P T A P W A L V S R E E A T L R A L R L CGCTGACCTTCTTGGCGCTTGGCGGACCTTTCAGGCGGCACTCTCCAGAGTGGCTCCAGAGTGGCTCCGAGCGCCGCTGGCGGCTGGCTTCCGCGAAGAGCTACGCTTACAGCTTCTGCTG
		-----A-----
S-Lab SR	1125	A E A V N C P H D A T K L S D A V E C L R T K D P N E L V D N E W G T L G I C E F P GCGAGCGCTCACTTCCGACCATGCGACCAAGCTGAGCGATCCCGTCCGATGCGTCCGACCAAGGATCCGACGAGCTGGTGGACAACGAGTGGGACGCTGGGGATCTCCGAGTTCC
		-----T-----
S-Lab SR	1251	F V P V V D G A F L D E T P Q R S L A S G R F K K T D I L T G S N T E E G Y Y F I I GTTGCTTCCGCTTGTGGACGAGCGTTCTCTGATGACACACCGCAGCGTTGCTTGGCAGCGCGCTTCAAGAAAACGACATCTGACCGCCAGCAACACGAGGAGGTTACTACTTTATCA
		-----T-----
S-Lab SR	1375	Y Y L T E L L R K E E G V T V T R E E F L Q A V R E L N P Y V N G A A R Q A I V F TTTACTATCAACGAGCTGCTACGAAAGAGGAGCGGTCAACGAGGAGTTCCTACAGCGGTCCGCGAGTTGAATCCGTAGCTGAACCGTGGCGCCGCGCAGGCGCATGCTGTTCT
		-----T-----

Fig. 6B

1 80
KISUMU GAATGCCCATTTGTTGCCATAGATTGAATTTCTTGGTTGTTGTTGTTGTTGTTGTTTCTTTTGACATGTTTGTGTTGTT
YAO -----

160
A F F T P Y I G H G E S
KISUMU TTTTCTTTCTCTCTCTCTCTCT--CTGTGGTTCCAACATTTTACACCATATATAGGTACCGGTGAGT
YAO -----TT-----

240
M R I I D A E L G T L E H V H S G A T P R R R G L T
KISUMU CCGTACGAATTATAGATGCCGAGTTGGGCACGCTCGAGCATGTCCACAGTGGAGCAACGCCGCCGCCGACCGGTCTGAAG
YAO -----A-----

320
R R E S N S D
KISUMU AGCGCGAGTCCAACCTCGGTAAGTACGCGATTGGAAGTGGCGGGACGTTTACCCTGCCGTGTACTACAATGCACTTTAC
YAO -----A-----A-----C-----

400
A N D N D P L V V N T D K G R I R G I
KISUMU CCCCACGCACACGCACCGGCAGACCGCAACGACAACGATCGCTGGTGGTCAACACGGATAACGGCGGCATCCGCGGCAT
YAO -----

480
T V D A P S G K K V D V W L G I P Y A Q P P V G P L R
KISUMU TACCGTCGATGCCCGCAGCGCAAGAAGTGGACGTGTGGCTCGGCATTCCCTACGCCCGACCGCGGTCCGGCCGTTAC
YAO -----C-----C-----

560
F R H P R P A E K W T G V L N T T T P P N S C V Q I
KISUMU GGTTCGTCATCCGCGCGCGCGGAAAAGTGGACCGCGGTGCTGAACACGACCACACCGCCCAACAGCTGGGTGCAGATC
YAO -----

Amorce Ex3AGdir

640
V D T V F G D F P G A T M W N P N T P L S E D C L Y I
KISUMU GTGGACACCGTGTTCGGGACTTCCCGGCGCGACCATGTGGAACCCGAACACGCCCTGTCCGAGCACTGTCTGTACAT
YAO -----

Amorce Ex3AGdir

Fig. 9A

720

N V V A P R P R P K N A A V M L W I F G G G F Y S G T
KISUMU TAACGTGGTGGCACCACCGACCCCGGCCAAGAATGCCGCCGTGCTGTGGATCTTCGGCGGCCTTCTACTCCGGCA
YAO -----G-----

800

A T L D V Y D H R A L A S E E N V I V V S L Q Y R V
KISUMU CCGCCACCTGGACGTGTACGACCACCGGCGCTTGCGTCGGAGGAGAACGTGATCGTGGTGTCCGTCCAGTACCGCGTG
YAO -----

880

A S L G F L F L G T P E A P G N A G L F D Q N L A L R
KISUMU CCCAGTCTGGGCTTCCTGTTTCTCGGCACCCCGGAAGCCCGGCAATGCCGACTGTTGATCAGAACCTTGCGCTACG
YAO -----

960

G T A G G T G T C T T T G C A T G C G T A A T G A G G G T A T A G T A T T C T A A C G A G G T G C T C T T C C C A T C A C T T C T T G G G A G T C A G C
KISUMU GTAGGTGTCTTTGCATGGGTGAATGAGGGTATAGTATTCTAACGAGGTGCTCTTCTTCCCATCACTTCTTGGGAGTCAGC
YAO -----G--T--TC--TA-T-----

1040

W V R D N I H R F G G D P S R V T L F G E S A G A V S
KISUMU TGGGTGGCGGACAACATTACCGGTTTCGGTGGTGATCGGTGGGTGTGACACTGTTGGGCGAGAGTCCCGGTGCGGTCTC
YAO -----

1120

V S L H L L S A L S R D L F Q R A I L Q S G S P T A P
KISUMU GGTGTGGTGCATCTGCTGTCCGCCCTGTCCCGCATCTGTTCCAGCGGGCATCTCCAGAGCGGCTCCCGACGCCAC
YAO -----T-----

Amorce Ex3AGrev

1200

W A L V S R E E A T L R
KISUMU CGTGGGCATTGGTATCGCGGAGGAAGCCACGCTAAGGTACGTGCCAGCTGCTGCTTTCCCAAACCAACCCCGGAC
YAO -----A-----

1280

A L R L A E A V G C P H
KISUMU AGCTCACACAACCTCTTTTCCTTGGCTCTTTTCTCGCTCCAGAGCACTGGGTTGGCCGAGCGGTCGGCTGCCCGCAC
YAO -----G-----

1360

E P S K L S D A V E C L R G K D P H V L V N N E W G T
KISUMU GAACCGAGCAAGCTGAGCGATGGGTCCAGTGTCTGCGCGCAAGGATCCGCACGTCTGGTCAACAACGAGTGGGGCAC
YAO -----

Fig. 9B

1440
L G I C E F P F V P V V D G A F L D E T P Q R S L A S
KISUMU GCTCGGCATTTCGCGAGTTCCCGTTGTCGCGGTGGTCCGACGGTCCGTTCTGGAACGACGCGCGCAGCGTTCCCTCGCCA
YAO -----

1520
G R F K K T E I L T G S N T E E G Y Y F I I Y Y L T
KISUMU CGCGGCGCTTCAAGAAGACGCGAGATCCTCACCGGCAGCAACACGAGGAGGCTACTACTTCATCATCTACTACCTGACC
YAO -----

1600
E L L R K E E G V T V T R E E F L Q A V R E L N P Y V
KISUMU GAGCTGCTCGCGAAGGAGGAGGCGGTGACCGTGACCGCGGAGGAGTTCTGCGAGGCGGTGCGCGAGCTCAACCGCTACGT
YAO -----

1680
N G A A R Q A I V F E Y T D W T E P D N P N S N R D A
KISUMU GAACGGCGCGCGCGCGCAGGCGATCGTGTTCCGAGTACACCGACTGACCGAGCGCGGACAACCGGAACAGCAACCGCGAGC
YAO -----

1760
L D K M V G D Y H F T C N V N E F A Q R Y A E E G N
KISUMU CGCTGGACAAGATGGTGGGCGACTATCACTTCACCTGCAACGTGAACGAGTTCCGCGAGCGGTACGCGGAGGAGCGCAAC
YAO -----

1840
N V Y M Y L Y T H R S K G N P W P R W T G V M H G D E
KISUMU AAGTCTACATGTATCTGTACACGCACCGCAGCAAAAGSCAAACCGGTGCGCGCGCTGGACGCGCGTGATGCAACGCGCAGCA
YAO -----

1920
I N Y V F G E P L N P T L G Y T E D E K D F S R K I M
KISUMU GATCAACTACGTGTTCCGCGAACCGCTCAACCCACCCTCGGCTACACCGAGGACGAGAAACACTTTAGCCGGAAGATCA
YAO -----

2000
R Y W S N F A K T G
KISUMU TGGGATACTGGTCTAACTTTGCCAAAACCGGTAAGTGTGTGTGTGTGTGTGTGTCAAACACCAGAGTGTGATCGCTCT
YAO -----A---C-A-A-----

2080
N P N P N T A S S E F P E W P K H T
KISUMU AACGCC-----TTCTCTCTTCAACAGCAATCCAAATCCCAACACGCGCCAGCAGCGAATTCGCCGAGTGGCCCAAGCACA
YAO ----A--AGCGTC-----T-----A-----

Fig. 9C

2160

A H G R H Y L E L G L N T S F V G R G P R L R Q C A

KISUMU CCGCCCACGGACCGCACTATCTGGAGCTGGGCCTCAACAGTCCTTCGTCGCTCGGGGCCACGGTTGAGGCAGTGTGCC
YAO -----

2240

F W K K Y L P Q L V A A T S

KISUMU TTCTGGAAGAAGTACCTTCCCCAGCTAGTTCCAGCTAOCCTGTAAGTCTCGT-GCAGCGCTTGAAATCCTCTCCCGCATCC
YAO -----A-T-T-A-CA---C-C---T---G---

2320

N L P G

KISUMU TCAACAGGGTCCAGGTTGCAATAACAAATGTATCTCTCTCTCTCTCAGTCTCTTTTCCCCAAAACAGCGAACCTACCAG
YAO C--T-----A-A-----A-----

2400

P A P P S E P C E S S A F F Y R P D L I V L L V S L

KISUMU GGCCAGCACCGCCCACTGAACCGTCCGAAAGCAGCGCATTTTTTTACCGACCTGATCTGATCGTGCCTGGTGTGCTG
YAO -----

2480

L T A T V R F I Q *

KISUMU CTTACGGCGACCGTCAGATTACATAATAATTACTACCCCATCCATGGCCTAGTTCTTTTAAGCTTTAAGATAGTCAGGA
YAO -----G-----

KISUMU ACAAATTTTTCTAACCAATTTCCCAACCCCTTTAGAGCAGAACCGAGGGAGAGATAGGACT
YAO -----

Fig. 9D

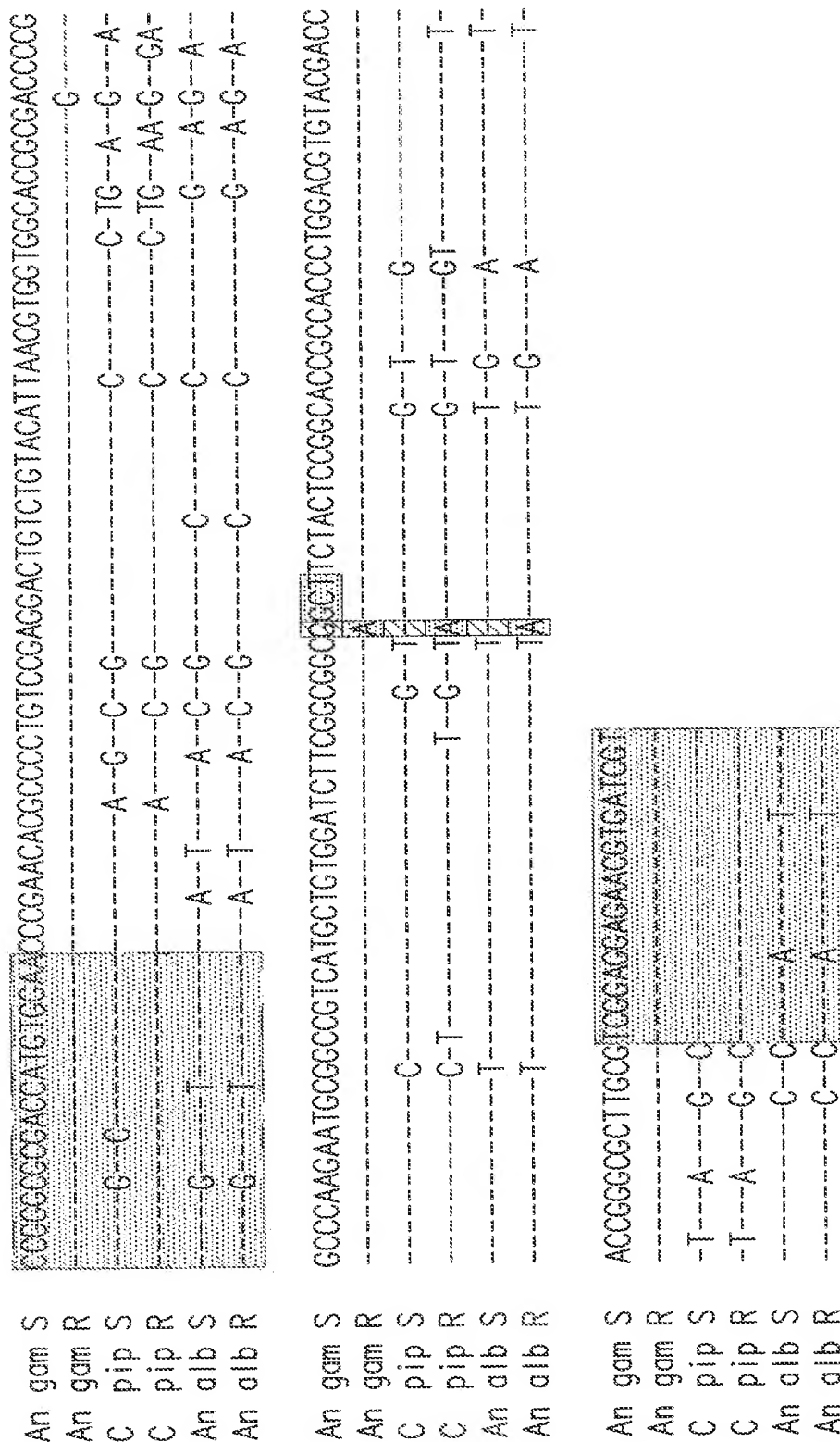


Fig. 13

>An. albi. "S"
CCGGGGCGGACTATGTGGAGCCCAATACGCCACACTCGGAGGACTGCCCTGTACATCAACGTGGTGGCGCGAGCCACGCCCAAGAAATGCTGCCGTCAATGCTGTGGATCTTCGG
CCGTGGCTTCTACTCCGGTACGGCCACACTGGAGGTACGATCAACGGGGGCTGCCCTGGGAAGAGAAGCTTATCGT

>An. albi. "R"
CCGGGGCGGACTATGTGGAGCCCAATACGCCACACTCGGAGGACTGCCCTGTACATCAACGTGGTGGCGCGAGCCACGCCCAAGAAATGCTGCCGTCAATGCTGTGGATCTTCGG
CCGTAGCTTCTACTCCGGTACGGCCACACTGGAGGTACGATCAACGGGGGCTGCCCTGGGAAGAGAAGCTTATCGT

Fig. 14